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M protein - protein search, using sw model

un on: March 7, 2005, 21:32:16 ; Search time 43 Seconds
(without alignments)
maximum DB seq length: 0
Maximum Match 0%
Listed first 45 summaries

ost-processing: Minimum Match 0%
Maximum Match 100%

total number of hits satisfying chosen parameters: 513545

ALIGNMENTS

Result No.	Score	Query	Length	DB	ID	Description
1	1879	100.0	364	4	US-10-166-606-4	Sequence 4, Appli
2	1589	84.6	346	2	US-08-613-220B-4	Sequence 4, Appli
3	140.5	7.5	647	1	US-07-894-212A-8	Sequence 8, Appli
4	140.5	7.5	649	1	US-07-894-212A-2	Sequence 2, Appli
5	140.5	7.5	650	1	US-07-893-928A-1	Sequence 1, Appli
6	105	227	4	US-09-107-532A-5554	Sequence 5554, AP	
7	101.5	5.6	360	4	US-09-710-279-2150	Sequence 2150, AP
8	101.5	5.4	376	4	US-09-710-279-2106	Sequence 2106, AP
9	101	5.4	329	1	US-08-270-013B-2	Sequence 2, Appli
10	97	5.2	653	4	US-09-540-236-3128	Sequence 3128, AP
11	97	5.2	653	4	US-09-540-236-3128	Sequence 3128, AP
12	94.5	5.0	367	3	US-09-134-001C-3678	Sequence 3678, AP
13	92	4.9	375	4	US-09-710-279-1840	Sequence 1840, AP
14	92	4.9	845	4	US-09-248-796A-15394	Sequence 15394, A
15	91.5	4.9	741	4	US-09-252-991A-31448	Sequence 31448, A
16	91.5	4.9	1009	4	US-09-693-146-4	Sequence 4, Appli
17	91	4.8	1031	4	US-09-543-681A-8245	Sequence 8245, AP
18	90.5	4.8	406	3	US-09-134-001C-3570	Sequence 3570, AP
19	90.5	4.8	789	4	US-09-248-796A-19294	Sequence 19294, A
20	90.5	4.8	1171	4	US-09-248-796A-16043	Sequence 16043, A
21	90	4.8	3854	4	US-09-949-016-7876	Sequence 7876, AP
22	89.5	4.8	322	4	US-09-489-039A-12383	Sequence 12383, A
23	89	4.7	857	4	US-09-248-796A-20522	Sequence 20522, A
24	88.5	4.7	399	4	US-09-252-991A-23741	Sequence 23741, A
25	88.5	4.7	764	3	US-09-235-451-36	Sequence 36, APPL
26	88.5	4.7	764	4	US-09-978-303-36	Sequence 36, APPL
27	88.5	4.7	993	4	US-09-894-998A-50	Sequence 50, APPL

RESULT 1
US-10-166-606-4
; Sequence 4, Application US/10166606
; Patent No. 6644756
; GENERAL INFORMATION:
; APPLICANT: Murphy, Dennis
; APPLICANT: Reid, John
; TITLE OF INVENTION: ALPHA GALACTOSIDASES AND METHODS FOR
; MAKING AND USING THEM (Amended)
; FILE REFERENCE: 09010-004005
; CURRENT APPLICATION NUMBER: US/10/166,606
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/407,806
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 08/613,220
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus

US-10-166-606-4

Query Match 100.0%; Score 1879; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 5.2e-191;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRALVFHGNLQYAEIPKSEIPKVIKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDID 60
Db 1 LRALVFHGNLQYAEIPKSEIPKVIKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDID 60

QY 61 LVKGIGIASDLIEIIGTSYTHAILPLPLPSRVEAQVQRDREVKEELFEVSPKGFWLPELAY 120
Db 61 LVKGIGIASDLIEIIGTSYTHAILPLPLPSRVEAQVQRDREVKEELFEVSPKGFWLPELAY 120

QY 121 DPITPAILKONGYEYLADGEAMLFSAHNSAIKPKIPLYPHLKAOREKRFRYIISYLIG 180
Db 121 DPITPAILKONGYEYLADGEAMLFSAHNSAIKPKIPLYPHLKAOREKRFRYIISYLIG 180

QY 181 LRELRAKAIKVFBGKVTLKAVKOIEAVPVWAVENTAVMLGIGRLPLMNPKKVASYIEDKD 240
Db 181 LRELRAKAIKVFBGKVTLKAVKOIEAVPVWAVENTAVMLGIGRLPLMNPKKVASYIEDKD 240

QY 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSLKHSGREYLRTSSWAP 300
Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSLKHSGREYLRTSSWAP 300

QY 301 DKSRIWREDEGNARLMLSYMRGELAFLAENSDAWRGEPERRLDAFRAIYNDRGE 360
Db 301 DKSRIWREDEGNARLMLSYMRGELAFLAENSDAWRGEPERRLDAFRAIYNDRGE 360

Db 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRIDAFA RAIYNDWRGE 360
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 2
 US-08-613-220B-4
 ; Sequence 4, Application US/08613220B
 ; Patent No. 5958751
 GENERAL INFORMATION:
 APPLICANT: Murphy, Dennis
 TITLE OF INVENTION: ALPHA-GALACTOSIDASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/613,220B
 FILING DATE: 08-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 09010/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-678-5070
 TELEFAX: 619-68-5099
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 TOPLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-613-220B-4

Query Match 84.6%; Score 1589; DB 2; Length 346;
 Best Local Similarity 95.1%; Pred. No. 3.3e-160;
 Matches 346; Conservative 0; Mismatches 0; Indels 18; Gaps 18;

Qy 1 LRALVFHGNLQYAEIPKSEIPKVIKEAYIPIVIEITLKEEIPFGLNITGYTLKFLPKDID 60
 Db 1 LRALVFHGNLQYAEIPKSE-PKVIEKAYIPIVIEITLKEE-PFGLNITGYTLKFLPKDII- 57

Qy 61 LVKGIGIASDLIEIIGTSYTHAILPLPLSRVEAQVORDREVKEELFEVSPKGFWLPELAY 120
 Db 58 LVKGIGIASDLIEIIGTSY-TAILPLPLSRVEAQVORDR-VKEELFEVSPKGFWLPELA- 114

Qy 121 DPTIPAILKDNGYELYLFADGEAMLFSAHNSAIKPKIPLYPHLIKQAREKRFRYISYLIG 180
 Db 115 DPTIPAILKDNGYELYLFAD-BAMLFSAHNSAIKPKIPL-PHLIKQAREKRFRYISYLL- 171

Qy 181 LRELKAIAKLVFECKVTLKAVDIEAVPVWA VNTAVMLGIGRLPLMNPKKVASHEDKD 240
 Db 172 LRELKAIAKLVFECKVTLK-VKDI EAVPVWA VNTAVML-IGRLPLMNPKKVASHEDKD- 228

Qy 241 NILYGTDIEFIGYRDIA GYRMSVEGLLEVIDELSELCLPSELKHSGRELYLRTSSWAP 300

Db 229 NILLYGTDIEFIGYRDIA GYRMSVEGLLEVIDELSELCLPSELKHSGRELYLRTSSWAP- 285
 Qy 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRIDAFA RAIYNDWRGE 360
 Db 286 DKSLRIWREDEGNARLNML-YNMRGELAFLAENS DARGW-PLPERRIDAFA RAIYNDWRG- 342

RESULT 3
 US-07-894-212A-8
 ; Sequence 8, Application US/07894212A
 ; Patent No. 5366883
 GENERAL INFORMATION:
 APPLICANT: ASADA, KIYozo
 APPLICANT: UEMORI, TAKashi
 APPLICANT: MUKAI, HIRoyuki
 APPLICANT: KATO, IKUNOSHIN
 APPLICANT: LADERMAN, KENNETH
 APPLICANT: ANFINSEN, CHRISTIAN
 TITLE OF INVENTION: THE ALPHA-AMYLASE GENE
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON, D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/894,212A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16773
 REFERENCE/DOCKET NUMBER: 95469/C-1195
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 647 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPLOGY: linear
 MOLECULE TYPE: protein
 US-07-894-212A-8

Query Match 7.5%; Score 140.5; DB 1; Length 647;
 Best Local Similarity 22.8%; Pred. No. 9.3e-06;
 Matches 89; Conservative 60; Mismatches 127; Indels 115; Gaps 23;

Qy 25 EKAYIPIVIEITLKEEIP---FGLNITGYTLKFLP---KOIDLVKGIGIASDLIEIIGTSY 78
 Db 27 EKCYWPFLETL--EEYPNMKVAIHTSGPLIEWLQDNRPEYIDLRLSVKRGQVEIWAGF 84

Qy 79 THAILPLPLSRVEAQVORDREVKE--ELFEVSPKGFWLPELAYDPTIPAILKDNGYELY 136
 Db 85 YEPVLASIP---KEDRIEQIRLMKEWAKSIGFDARGWLTERVWQPELVTKLKGESGDY 141

Qy 37 FADGEAMLFSAHNSAIKPKIPLY-PHLIKQARE-----KFRYISYLLGLRELRKA 187
 Db 142 IVD----DYHFMSAGLSKEELYWPyT TEDGEVIAVFPIDEKL--XLI PFRPVDKV 192

QY 188 IKL---VFEKGKTLKAV--KDIIEAVPVWVAVTAVMLGIGRLPLMNPKKVASWI----- 236
 Db 193 LEYLHSLIDGDESKVAVFHDDGEKFGIWPGBTYEWY-----EKGWLREFEDR 239
 QY 237 ---EDKDNLILYGTDIE----FIGYRDIAGYRMSVEGLLEVIDELNSELCLP----- 281
 Db 240 ISSDEKINLMLYTEYLEKYKPRGLVYLPIASY----FEM----SEWSLPAKQARLF 287
 QY 282 ---SELKHSG---RELYLRTSSWAPDKSLRIWREDEGN---ARLNMLSYNMRGELAFL 330
 Db 288 VEFVNELKVKGIFEEKYRFVRGGIW---KNF-FYKYPESENVMHKRMLMVKLVNN--- 339
 QY 331 AENSDARGWEPLPERRLDAFRAIYND--WRG 359
 Db 340 -----PEARKYLLRAQCNDAYWHG 358

RESULT 4

US-07-894-212A-2

; Sequence 2, Application US/07894212A
 ; Patent No. 5366883

GENERAL INFORMATION:

APPLICANT: ASADA, KIYOSO
 APPLICANT: UEMORI, TAKASHI
 APPLICANT: MUKAI, HIROYUKI
 APPLICANT: KATO, IKUNOSHIN
 APPLICANT: LADERMAN, KENNETH
 APPLICANT: ANFINSEN, CHRISTIAN

TITLE OF INVENTION: THE ALPHA-AMYLASE GENE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON, D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/894, 212A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16773

REFERENCE/DOCKET NUMBER: 95469/C-1195

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 649 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-894-212A-2

Query Match 7.5%; Score 140.5; DB 1; Length 649;
 Best Local Similarity 22.8%; Pred. No. 9.4e-06;
 Matches 89; Conservative 60; Mismatches 127; Indels 115; Gaps 23;

QY 25 EKAYIPVIETLIKEEIP--FGINITGYTLKFLP--KDIIDLVKGGIASDLIEIGTSY 78
 Db 29 EKCYWPFLETL--EYYPNMKVAIHTSGPLIEWLQDNRPEYIDLLRSVLVRGQVEIVVAGF 86

QY 79 THAILPLPLSRVEAQVORDREVKE--ELFEVSPKGFWLPELAYDPIIPAILKDNGYEYL 136
 Db 87 YEPVLASIP--KEDRIOQIRLMKEWAKSIGFDARGVNLTERVWQPELVKTLKESGIDYV 143

RESULT 5

US-07-893-928A-1

; Sequence 1, Application US/07893928A
 ; Patent No. 5578479

GENERAL INFORMATION:

APPLICANT: LADERMAN, KENNETH
 APPLICANT: ANFINSEN, CHRISTIAN
 TITLE OF INVENTION: a-AMYLASE FROM HYPERTHERMOPHILIC
 TITLE OF INVENTION: ARCHAEBACTERIUM
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON, D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Tape

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/893, 928A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16773

REFERENCE/DOCKET NUMBER: 95470/C-1197

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 650 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-893-928A-1

Query Match 7.5%; Score 140.5; DB 1; Length 650;
 Best Local Similarity 22.8%; Pred. No. 9.4e-06;
 Matches 89; Conservative 60; Mismatches 127; Indels 115; Gaps 23;

QY 25 EKAYIPVIETLIKEEIP--FGINITGYTLKFLP--KDIIDLVKGGIASDLIEIGTSY 78
 Db 29 EKCYWPFLETL--EYYPNMKVAIHTSGPLIEWLQDNRPEYIDLLRSVLVRGQVEIVVAGF 86

QY 79 THAILPLPLSRVEAQVORDREVKE--ELFEVSPKGFWLPELAYDPIIPAILKDNGYEYL 136
 Db 87 YEPVLASIP--KEDRIOQIRLMKEWAKSIGFDARGVNLTERVWQPELVKTLKESGIDYV 143

Db 87 YEPVYLASIP---KEDRIEQTIRLMKEWAKSIGFDARGWLTTERVWOPENLVKTLKESGIDY 143
 Qy 137 FADGEAMLFSAHNSAIKPIKPLY-PHLIKAQRE-----KFRYISYLLGLRELRK 187
 Db 144 IVD-----DYHFMSAGLSKEEYLWPPYTEDGGEVIAFPIDEKLRL--YLIPFRPDKV 194
 Qy 188 IKL---VFEGKVTLKAV--KDIIEAVPVWVAINTAVMLGIGRLPLMNPKKVASWI---- 236
 Db 195 LEYIHLISLIDGDESKVAVFHDDGEKFGIWPGTYEWY-----EKGWLREFFDR 241
 Qy 237 ---EDKDNTILLYGTDIE----FIGYRDIAGYRMSVEGLLEVIDEELNSELCLP---- 281
 Db 242 ISSDEKINLMLYTEYLEKVKPRGLVULPIASY-----FEM-----SEWSLPAKQARLF 289
 Qy 282 ---SELKHSG---RELYLRTSSWAPDKSLRIWREDEGN---ARLNMLSYNMRGELAFL 330
 Db 290 VEFVNELKVKGIFEKYRFVRGGIW--KNF-FYKVPESNYMHKRMLMVKLVRNN--- 341
 Qy 331 AENS DARGWEPPLPERRLDAFRAIYND--WRG 359
 Db 342 -----PEARKYLLRAQCNDAYWHG 360

RESULT 6

US-09-107-532A-5554

; Sequence 5554, Application US/09107532A
 ; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5554:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1..227
 SEQUENCE DESCRIPTION: SEQ ID NO: 5554:

RESULT 7

US-09-710-279-2150

; Sequence 2150, Application US/09710279
 ; Patent No. 6703492

GENERAL INFORMATION:

APPLICANT: KIMMELLY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERmidis NUCLEIC ACIDS AND PROTEINS
 FILE REFERENCE: PU3480US
 CURRENT APPLICATION NUMBER: US/09/710,279
 CURRENT FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 60/164,258
 PRIOR FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2150

LENGTH: 360

TYPE: .RRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: amino acid sequence

US-09-710-279-2150

RESULT 8

US-09-107-532A-5554

; Query Match 5.6%; Score 105; DB 4; Length 227;
 Best Local Similarity 24.2%; Pred. No. 0.01; Gaps 12;
 Matches 60; Conservative 34; Mismatches 88; Indels 66; Gaps 12;

Matches 57; Conservative 52; Mismatches 117; Indels 73; Gaps 12;

Matched 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved 52; MisMatched 117; Indels 73; Gaps 12;

Score 101.5; DB 4; Length 360;

Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 12;

Matches 57; Conserved

RESULT 8
US-09-710-279-2106
; Sequence 2106, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2106
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-710-279-2106

Query Match 5.4%; Score 101.5; DB 4; Length 376;
Best Local Similarity 19.1%; Pred. No. 0.054; Matches 57; Conservative 52; Mismatches 117; Indels 73; Gaps 12;

Qy 4 LVFFHGNLQYEAIPKSEIPKVIKEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIDLVVK 63
Db 47 LIFKG-----VKRIVEDGYGSIIRKLIONNI--NLIALHTNLDVNPKGVNRMLA 93

Qy 64 GGIASDLIEIGT-SYTHAILPLPLRSRVEAQVORDREKEELFEVSPKGFWLPELAYD 121
Db 94 DQIGLENISMINTNSSYYKVOTPIPKNYE-----DFKDSLNL----- 133

Qy 122 PIPIAILKDNQGYEYLADGEAMLFSAHNSAIKPIKLYPHLKAQREKRFRYISVLGL 181
Db 134 ---GLAKEGYEYCFSEG-----KGQFKPVGDAASPYIGKLDS-----IEVV--- 173

Qy 182 RELRKAIALVF----BGKVTLKAWKDIE--AVPV--WVAVNTAVMLGIGRLPLMNPKKV 232
Db 174 ---DETKELEFMIKDNELIETKRAILDNHPYETPVFDFIKMNKESEYGLGIGTQLNQMT 229

Qy 233 ASWIEDKONILLYGTIDFIGYRDIAGYRMSVEGLLEV----IDELNSELCLPSELKH 286
Db 230 LDEFSEYAKKQLNIPSVRYTGQHDSPIKKVAIIGGGIGFEYKASQLGADVFTGDIK 288

RESULT 9
US-08-270-013B-2
; Sequence 2, Application US/08270013B
; Patent No. 5686294
; GENERAL INFORMATION:
; APPLICANT: Sogabe et al.
; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,418
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,013
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 164701/1993
; FILING DATE: 02-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Allen E.
; REGISTRATION NUMBER: 37354

FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Green, Robert F.
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 62321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEX: (253) 3533
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-270-013B-2

Query Match 5.4%; Score 101; DB 1; Length 329;
Best Local Similarity 25.3%; Pred. No. 0.05; Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

Qy 10 LQYAEIIPKSEIPK-----VIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIDL 61
Db 130 MTYTTFKESGFPKRNVRIGQSGVLDTAR---FRTFVABE---LNIS-----VKDVTFP 175

Qy 62 VKGGIASDLIEIGTSYTHAI-LPLPLRSRVEAQVORDREKEELFEVSPKG-FWLPE 117
Db 176 VLGGHGDDMVPLVRYSYAGGIPLEKLIPKDRLDIAVERTRKGGEIVNLNGNSAYAPA 235

Qy 118 LAYDPIIPAILKDN-----GYEYLF 137
Db 236 ASLIVEMVEAILKDQRRILPAIAYLEGEBYGVGYIY 269

RESULT 10
US-08-838-418-2
; Sequence 2, Application US/08838418
; Patent No. 5744342
; GENERAL INFORMATION:
; APPLICANT: Sogabe et al.
; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,418
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,013
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 164701/1993
; FILING DATE: 02-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Allen E.
; REGISTRATION NUMBER: 37354

REFERENCE/DOCKET NUMBER: 78339
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5600
 TELEFAX: (312) 616-5700
 TELEX: (25) 3533

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 329 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-418-2

Query Match 5.4%; Score 101; DB 1; Length 329;
 Best Local Similarity 25.3%; Pred. No. 0.05;
 Matches 39; Conservative 25; Mismatches 50; Indels 40; Gaps 7;

Qy 10 LQYAEIPIKSEIPK-----VIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIDL 61
 Db 130 MTYTIVFKESGFPKNRVIQGSQGVLDTAR--FRFVAAE---LNTS-----VKDVTF 175

Qy 62 VKGIGIASDLEIIGTSYTHAI-LPLPLSRVEAQVORDREVKEELFEVSPKG--FWLPE 117
 Db 176 VLGE3HGDMDMVELVRYSYAGGIPLEKLIPKDRDAIVERTRKGGEIVNLNGNSAYYAPA 235

Qy 118 LAYOPIIPIAIIKDN-----GYEYL 137
 Db 236 ASLIVEMVEAIIKDKQRRLIPAIAYLEGYEGYEGIY 269

RESULT 11
 US-09-540-236-3128
 ; Sequence 3128, Application US/09540236
 ; Patent No. 6673910

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS

FILE REFERENCE: 2709.2005-001
 CURRENT APPLICATION NUMBER: US/09/540,236
 CURRENT FILING DATE: 2000-04-04
 NUMBER OF SEQ ID NOS: 3840
 SEQ ID NO 3128
 LENGTH: 653
 TYPE: PRT
 ORGANISM: *M. catarrhalis*
 US-09-540-236-3128

Query Match 5.0%; Score 94.5; DB 3; Length 367;
 Best Local Similarity 18.7%; Pred. No. 0.29;
 Matches 56; Conservative 52; Mismatches 118; Indels 73; Gaps 12;

Qy 4 LVFHGNLQYARIPKSEIPKVIKEAYIPVIETLIKEIPFGLNITGYTLKFLPKDIDLVK 63
 Db 68 LIFKG-----VKRIVEDGYGSIIRKLIQNNI--NLIALHTNLDVNPKGVNRMLA 114

Qy 64 GGIASDLEIIGT-SYTHAILPLPLSRVEAQVORDREVKEELFEVSPKGFWLPBELAYD 121
 Db 115 DQIGLENISMINTSSYYKVQTIPKVNIE-----DFKDSLNL----- 154

Qy 122 PIPIAIIKDNGYEYLFDAGEAMLSAHINSAIKPIKLYPHLIKQREKRFRYISYLLGL 181
 Db 155 ---GLAKEGNYEYCFSEEG-----KGQFGPVGADSPYIKLDS-----IEYV-- 194

Qy 182 RELRAIAKLVF---EGKVTLKAVKDIE--AVPV--WAVNTAVMLGIGRLPLMNPKV 232
 Db 195 ---DEIKLEFMKDNLEITKRAILDNHPYETPVDFFIKMNESEYGLGIIGQLNQNT 250

Qy 233 ASWIEDKDNLILYGTIDFIGYRDIAGYRMSVEGLLEV----IDELNSELCLCPSELKH 286
 Db 251 LDEFSEYAKKQNLIPSVRYTGQHDSPPIKKVAIIGGSGIGFEYKASQLGADVFTGDIKH 309

Query Match 5.2%; Score 97; DB 4; Length 653;
 Best Local Similarity 21.9%; Pred. No. 0.4;
 Matches 72; Conservative 43; Mismatches 128; Indels 86; Gaps 13;

Qy 22 KVIKEKAYIPVIETLIKEEIPFGLNITGYTLKFLP-----KDIIDLVKGGIAS--- 68
 Db 95 KRIEPAYRGVITD--REGAPLAANAPLYTVFFDPYAYEEYVLDNETKTKSETAKQKA 152

Qy 69 -----DLIBIIGTSYTHAILPLPLSRVEAQVORD-----REVKEELFEVSPKG 113
 Db 153 LKKLKEMDLVRL-----AAAANYPLEKLEAVGIDHTLTSNSQKVEAL---PKGA 201

Qy 114 WLEPLA-YDPIIPIAIIKDNGLNGYEYLFDAGEAMLSAHINSAIKPIKLYPHLIKQREKR 172
 Db 202 SSRRRLVLLNRSPEVAKSVDLGLFAIGREQFYQRYLQA-EPAQOLLGMAQSDETQG 260

Qy 173 RYISYLLGLRELRAIAKLVFEGKVTLKAVKDIEAVPVWAVNTAVMLGIGRLPLMNPKV 232
 Db 261 GYIG-----RAGIEAKYNERLAGKDGK-----VOILRGTGROPIOEIQI 300

Qy 233 ASWIEDKDNLILYGTIDFIGYRDIAGYRMSVEGLLEV----IDELNSELCLCPSELKH 292
 Db 301 EPLIEGENIRLTIDSRLQVYLYKE-----LEQVGRLO-----SARSSGMVVD 343

Qy 293 LRT-----SSWAPDKSLRIWREDEGNAR 315

RESULT 12
 US-09-134-001C-3678
 Sequence 3678, Application US/09134001C
 Patent No. 6380370

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134, 001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064, 964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055, 779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 3678
 LENGTH: 367
 TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-3678

Query Match 5.0%; Score 94.5; DB 3; Length 367;
 Best Local Similarity 18.7%; Pred. No. 0.29;
 Matches 56; Conservative 52; Mismatches 118; Indels 73; Gaps 12;

Qy 4 LVFHGNLQYARIPKSEIPKVIKEAYIPVIETLIKEIPFGLNITGYTLKFLPKDIDLVK 63
 Db 68 LIFKG-----VKRIVEDGYGSIIRKLIQNNI--NLIALHTNLDVNPKGVNRMLA 114

Qy 64 GGIASDLEIIGT-SYTHAILPLPLSRVEAQVORDREVKEELFEVSPKGFWLPBELAYD 121
 Db 115 DQIGLENISMINTSSYYKVQTIPKVNIE-----DFKDSLNL----- 154

Qy 122 PIPIAIIKDNGYEYLFDAGEAMLSAHINSAIKPIKLYPHLIKQREKRFRYISYLLGL 181
 Db 155 ---GLAKEGNYEYCFSEEG-----KGQFGPVGADSPYIKLDS-----IEYV-- 194

Qy 182 RELRAIAKLVF---EGKVTLKAVKDIE--AVPV--WAVNTAVMLGIGRLPLMNPKV 232
 Db 195 ---DEIKLEFMKDNLEITKRAILDNHPYETPVDFFIKMNESEYGLGIIGQLNQNT 250

Qy 233 ASWIEDKDNLILYGTIDFIGYRDIAGYRMSVEGLLEV----IDELNSELCLCPSELKH 286
 Db 251 LDEFSEYAKKQNLIPSVRYTGQHDSPPIKKVAIIGGSGIGFEYKASQLGADVFTGDIKH 309

RESULT 13
 US-09-710-279-1840
 Sequence 1840, Application US/09710279
 Patent No. 6703492

GENERAL INFORMATION:
 APPLICANT: KIMMERLY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US
 CURRENT APPLICATION NUMBER: US/09/710, 279
 CURRENT FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 60/164, 258
 PRIOR FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1840
 LENGTH: 375
 TYPE: FRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: amino acid sequence
 US-09-710-279-1840

Query Match 4.9%; Score 92; DB 4; Length 375;
 Best Local Similarity 19.3%; Pred. No. 0.55; Mismatches 55; Indels 138; Gaps 16;
 Matches 72; Conservative 55; MisMatcheB 109; Indels 138; Gaps 16;

Qy 59 IDLVKGIGIASDLIEIIGTSYTHAILPLPLSRV---EAQVORDREVKEELFEVSPK--- 111
 Db 3 IDIESG---DFIAFIGHTSGSGKTTLRMINRMIESTEGEITIDGKNIKELNPVELRSSI 58

Qy 112 GFWLPELAYDP-----IIPAILK-----DNGYEYL----- 136
 Db 59 GYVIQQIGLMRPHMTVKENIVLVPKLKWQSKEKDEKAKELIRLVDLPEEYLDRYPSELSG 118

Qy 137 -----FADGEAMLFSAHLNSAIKPI-KPLYPHLIK--AORERKFRYVISYLLGL 181
 Db 119 GQQQRIGVVRALAAEQDILMDEPFGLDPITRDTLQDVLKQQLGKTFIFVTH---- 174

Qy 182 RELRKAIAL----- 203
 Db 175 -DMDEAIKLAQKICIMTNGQVIQYTDNILRSANDFVRDPFIGNRLLQDRPNRTVKD 233

Qy 204 IEAVPVWVAINTAVMLGIGRLPLMNPKVVASWIEDKDNLILLYGTDIEFIGYRDIAGYRMS 263
 Db 234 AMIKPVTVHVDRLSLNDAVN---IMREKRV----DTIFVVGNDHEHLLGYLDIEDINEG 283

Qy 264 VEGGLEVIDELNSELC---LPSELKHSGRELYLRTSSWAP----DKSL---- 304
 Db 284 LRHHKELIDTMQRDIYRVRIDSQDVSRTILKRNVRNVPVVDSDNKTILLGLVTRANLVD 343

Qy 305 ---RIWRE-DEGN 313
 Db 344 IVYDSIWEGELESGN 357

RESULT 14

US-09-248-796A-15394 Application US/09248796A
 ; Sequence 15394, Application US/09248796A
 ; Patent No. 6747137

; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 31448
 ; LENGTH: 741
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-31448

Query Match 4.9%; Score 91.5; DB 4; Length 741;
 Best Local Similarity 19.5%; Pred. No. 1.9; Mismatches 63; Indels 153; Gaps 22;
 Matches 84; Conservative 63; MisMatcheB 131; Indels 153; Gaps 22;

Qy 34 TLIKEEIPFGLNITGYTLKFLPKDIDLVKGIGIASDLIEIIGTSYTHAI-----LPLLP 87
 Db 257 TMWKSHPI---VFGHAVSVVYKDVF---KMG---QLFEEIGVNPNNGISSVYDKIKSLP 308

Qy 88 LSRVEAQVORDREVKEELFEV-----SPKG---PWLP-ELAYDPLIPAILKDNG 132
 Db 309 ASQQE-----EILHDIEHVYSHRPEMAMVDSVKGITNLHIPSVDASMPAMIRNSG 361

Qy 133 YEYLFDAG-----EAMLFSAHLNSAIKPIKPLYPHLIKAOREKFRY 174
 Db 362 -QWKGDKQDKTAKMPESTYARIYQEMINFCKTNAGFDPTTMGSVPVNGLMAQKAEY 420

Qy 175 ISYLGIGRELRLKAIALVFEKGVTLKAV-----KDIETAVPVWVAINTA-----VM 218
 Db 421 GSH-----DKTFEMTAG---TMRVVLADGSVLMQHDVETQTKDAPIRDWK 471

Qy 219 LGIGR-----LPLMN-----KKVASWIEDKDNLILLYGTDIEFIGYRDIAGYR 261
 Db 472 LAVTRARQSDTPAIFWLDPERAHDRERLKVELYLDHD---LTGLDISHMGYNE-AIR 526

Qy 262 MSVEGLLEVIDELN-----SEL-----CL 280

Db 527 VSMERLIRGKDTISVTGNGVRLDYTLDFPIMELGTSAKMLSIIVPLMAGGGMTEGAGGSA 586

Qy 281 PSELKHSGRELYLRTSSWAPDKSRLIWR-----EGNARLNLMSYNMRGELAFLNSDA 336

Qy 587 PKHVOOLVEENYLRWDLSLGEPLALAVSLEETGKTKGNAKAKLKGKALDEATGKLLDDNKS 646

Db 337 RGWEPLPERL 347

Db 647 -----PSRKV 651

Tue Mar 8 09:44:21 2005

us-09-619-032a-4.rai

Page 8

Search completed: March 7, 2005, 21:45:20
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 21:42:11 ; Search time 132 Seconds
(without alignments)
907.366 Million cell updates/

Title: US-09-619-032A-4
Perfect score: 1879
Sequence: 1 LRALVFHGNLOYAEIPKSEI.....RRLDAFRAYNDWRGENGEP 364

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA: *

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1870	99.5	364	9 US-09-886-400-4 Sequence 4,
2	1870	99.5	364	13 US-10-112-357-4 Sequence 4,
3	1870	99.5	364	13 US-10-114-403-4 Sequence 4,
4	1870	99.5	364	13 US-10-116-606-4 Sequence 4,
5	1870	99.5	364	13 US-10-112-331-4 Sequence 4,
6	1870	99.5	364	13 US-10-112-377-4 Sequence 4,
7	1870	99.5	364	13 US-10-116-581-4 Sequence 4,
8	1870	99.5	364	13 US-10-112-442-4 Sequence 4,
9	1870	99.5	364	13 US-10-112-418-4 Sequence 4,
10	1870	99.5	364	13 US-10-114-083-4 Sequence 4,
11	111.5	5.9	890	15 US-10-282-122A-53281 Sequence 53,
12	109	5.8	312	15 US-10-369-493-23237 Sequence 233,
13	105.5	5.6	573	15 US-10-424-599-175517 Sequence 175,

SUMMARIES

NO.	CODE	MATCH	DESIGN	DIS	TD	DESCRIPTION
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2	1870	99.5	364	13	US-10-112-357-4	Sequence 4, Appli
3	1870	99.5	364	13	US-10-114-403-4	Sequence 4, Appli
4	1870	99.5	364	13	US-10-116-606-4	Sequence 4, Appli
5	1870	99.5	364	13	US-10-112-331-4	Sequence 4, Appli
6	1870	99.5	364	13	US-10-112-377-4	Sequence 4, Appli
7	1870	99.5	364	13	US-10-116-581-4	Sequence 4, Appli
8	1870	99.5	364	13	US-10-112-442-4	Sequence 4, Appli
9	1870	99.5	364	13	US-10-112-418-4	Sequence 4, Appli
10	1870	99.5	364	13	US-10-114-083-4	Sequence 4, Appli
11	111.5	5.9	890	15	US-10-282-122A-53281	Sequence 53281, A
12	109	5.8	312	15	US-10-369-493-23237	Sequence 23237, A
13	105.5	5.6	573	15	US-10-424-599-175517	Sequence 175517,

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

ALIGNMENT

Sequence	12361, A
Sequence	5468, AP
Sequence	44391, A
Sequence	4506, AP
Sequence	7264, AP
Sequence	122721,
Sequence	17395, A
Sequence	47208, A
Sequence	56, APP
Sequence	63055, A
Sequence	20, APP
Sequence	37809, A
Sequence	58833, A
Sequence	69849, A
Sequence	10268, A
Sequence	77165, A
Sequence	122301,
Sequence	52807, A
Sequence	55460, A
Sequence	161607,
Sequence	9015, AP
Sequence	39, APP
Sequence	54582, A
Sequence	7195, AP
Sequence	20014, A
Sequence	71768, A
Sequence	167, APP
Sequence	197248,
Sequence	186073,
Sequence	186071,
Sequence	152, APP

Db 61 LVKGGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELFELSPKGFWLPELAY 120
 Qy 121 DPIPAILKDONGEYLFADGEAMLSAHLNSAIKPIKPLYPHLIKAQREKFRYISYLIG 180
 Db 121 DPIPAILKDONGEYLFADGEAMLSAHLNSAIKPIKPLYPHLIKAQREKFRYISYLIG 180
 Qy 181 LRELRAIKLVFEGKVTLKAVKDIAPVWVAINTAVMLGIGRLPLMNPKKVASWIEDKD 240
 Db 181 LRELRAIKLVFEGKVTLKAVKDIAPVWVAINTAVMLGIGRLPLMNPKKVASWIEDKD 240
 Qy 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
 Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
 Qy 301 DKSLSRIRWREDEGNARLNMLSYNMRGELAFLAENSARGWEPPLPERRLDAFRAYNDWRGE 360
 Db 301 DKSLSRIRWREDEGNARLNMLSYNMRGELAFLAENSARGWEPPLPERRLDAFRAYNDWRGE 360
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 2
 US-10-112-357-4
 ; Sequence 4, Application US/10112357
 ; Publication No. US20020115099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Ried, John
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE THEREOF
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/112,357
 ; CURRENT FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: 09/886,400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619,032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407,806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613,220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Thermococcus alcaliphilus
 ; US-10-114-403-4

Query Match Score 1870; DB 13; Length 364;
 Best Local Similarity 99.5%; Pred. No. 4.9e-165;
 Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFHGNLQYAEIPKSEIPKVIKEAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60
 Db 1 LRALVFHGNLQYAEIPKSEIPKVIKEAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60
 Qy 61 LVKGGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELFEVSPKGFWLPELAY 120
 Db 61 LVKGGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELFEVSPKGFWLPELAY 120
 Qy 121 DPIPAILKDONGEYLFADGEAMLSAHLNSAIKPIKPLYPHLIKAQREKFRYISYLIG 180
 Db 121 DPIPAILKDONGEYLFADGEAMLSAHLNSAIKPIKPLYPHLIKAQREKFRYISYLIG 180
 Qy 181 LRELRAIKLVFEGKVTLKAVKDIAPVWVAINTAVMLGIGRLPLMNPKKVASWIEDKD 240
 Db 181 LRELRAIKLVFEGKVTLKAVKDIAPVWVAINTAVMLGIGRLPLMNPKKVASWIEDKD 240
 Qy 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
 Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 3
 US-10-114-403-4
 ; Sequence 4, Application US/10114403
 ; Publication No. US20020115100A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Ried, John
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE THEREOF
 ; FILE REFERENCE: DIVER1120-4
 ; CURRENT APPLICATION NUMBER: US/10/114,403
 ; CURRENT FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 09/886,400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619,032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407,806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613,220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Thermococcus alcaliphilus
 ; US-10-114-403-4

Query Match Score 1870; DB 13; Length 364;
 Best Local Similarity 99.5%; Pred. No. 4.9e-165;
 Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFHGNLQYAEIPKSEIPKVIKEAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60
 Db 1 LRALVFHGNLQYAEIPKSEIPKVIKEAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60
 Qy 61 LVKGGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELFEVSPKGFWLPELAY 120
 Db 61 LVKGGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELFEVSPKGFWLPELAY 120
 Qy 121 DPIPAILKDONGEYLFADGEAMLSAHLNSAIKPIKPLYPHLIKAQREKFRYISYLIG 180
 Db 121 DPIPAILKDONGEYLFADGEAMLSAHLNSAIKPIKPLYPHLIKAQREKFRYISYLIG 180
 Qy 181 LRELRAIKLVFEGKVTLKAVKDIAPVWVAINTAVMLGIGRLPLMNPKKVASWIEDKD 240
 Db 181 LRELRAIKLVFEGKVTLKAVKDIAPVWVAINTAVMLGIGRLPLMNPKKVASWIEDKD 240
 Qy 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
 Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
 Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 4
 US-10-116-606-4
 ; Sequence 4, Application US/10116606
 ; Publication No. US20020119515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Ried, John
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
 ; CURRENT FILING DATE: 2002-04-03
 ; CURRENT APPLICATION NUMBER: US/10/116, 606
 ; PRIOR APPLICATION NUMBER: US/09/886, 400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619, 032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407, 806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613, 220
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 09/407, 806
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Thermococcus alcaliphilus
 ; US-10-116-606-4

Query Match 99.5%; Score 1870; DB 13; Length 364;
 Best Local Similarity 99.5%; Pred. No. 4.9e-165;
 Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFGHGNLQYAEIIPKSEIIPKVIKEKAYIPVIETLIKKEBIPFGLNITGYTLKFLPKDID 60
 Db 1 LRALVFGHGNLQYAEIIPKSEIIPKVIKEKAYIPVIETLIKKEIIPFGLNITGYTLKFLPKDID 60

Qy 61 LVKGIGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELPEVSPKGFWLPELAY 120
 Db 61 LVKGIGIASDLIEIIGTSYTHAILPLPLSRVEAQVQRDREVKEELPEVSPKGFWLPELAY 120

Qy 121 DPIIPAILKDNGEYELFADGEAMLFSAHNSAIKPIKPLYPHLIKAQREKRFRYISYLG 180
 Db 121 DPIIPAILKDNGEYELFADGEAMLFSAHNSAIKPIKPLYPHLIKAQREKRFRYISYLG 180

Qy 181 LRELRKAIKLVFEKGVTLKAVKDIEAVPVWAVNTAVMLGIGRLPLMNPKKVVASWIEDKD 240
 Db 181 LRELRKAIKLVFEKGVTLKAVKDIEAVPVWAVNTAVMLGIGRLPLMNPKKVVASWIEDKD 240

Qy 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLVIDELENSELCLPSELKHSGRELYLRTSSWAP 300
 Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLVIDELENSELCLPSELKHSGRELYLRTSSWAP 300

Qy 301 DKSLSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRLDAFRAIYNDWRGE 360
 Db 301 DKSLSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRLDAFRAIYNDWRGE 360

Qy 181 LRELRKAIKLVFEKGVTLKAVKDIEAVPVWAVNTAVMLGIGRLPLMNPKKVVASWIEDKD 240
 Db 181 LRELRKAIKLVFEKGVTLKAVKDIEAVPVWAVNTAVMLGIGRLPLMNPKKVVASWIEDKD 240

Qy 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLVIDELENSELCLPSELKHSGRELYLRTSSWAP 300
 Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLVIDELENSELCLPSELKHSGRELYLRTSSWAP 300

Qy 301 DKSLSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRLDAFRAIYNDWRGE 360
 Db 301 DKSLSRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRLDAFRAIYNDWRGE 360

Qy 361 NGEP 364
 Db 361 NGEP 364

RESULT 5
 US-10-112-331-4
 ; Sequence 4, Application US/10112331
 ; Publication No. US20020119550A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: Murphy, Dennis
 ; APPLICANT: Ried, John
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH
 ; CURRENT FILING DATE: 2002-03-29
 ; CURRENT APPLICATION NUMBER: US/10/112, 377
 ; PRIOR APPLICATION NUMBER: 09/886, 400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619, 032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407, 806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613, 220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 364

PRIOR APPLICATION NUMBER: US/09/886, 400
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 09/619, 032
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/407, 806
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 08/613, 220
 ; PRIOR FILING DATE: 1996-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 364

; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus
; US-10-112-377-4

Query Match 99.5%; Score 1870; DB 13; Length 364;
Best Local Similarity 99.5%; Pred. No. 4.9e-165;
Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFGNLOQAYAIPKSEIPKVIKAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60
Db 1 LRALVFGNLOQAYAIPKSEIPKVIKAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60

Qy 61 LVKGIGIASDLIEIIGTSYTHAILPLPLPSRVEAQORDREVKEELFEVSPKGFWLPBELAY 120
Db 61 LVKGIGIASDLIEIIGTSYTHAILPLPLPSRVEAQORDREVKEELFEVSPKGFWLPBELAY 120

Qy 121 DP1PAIKDNGYEYLADGEAMLFSAHNSAIKPKPLYPHILKAOREKRFRYISYLLG 180
Db 121 DP1PAIKDNGYEYLADGEAMLFSAHNSAIKPKPLYPHILKAOREKRFRYISYLLG 180

Qy 181 LRELRAIAKLVLFEKGVTLKAVKDIIEAVPVWAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240
Db 181 LRELRAIAKLVLFEKGVTLKAVKDIIEAVPVWAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240

Qy 241 NILLYGTDIEFIGYRDIGYRMSVEGLLEVIDELNSECLPSELKHSGRELYLTSSWAP 300
Db 241 NILLYGTDIEFIGYRDIGYRMSVEGLLEVIDELNSECLPSELKHSGRELYLTSSWAP 300

Qy 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERRLDAFRAYNDWRGE 360
Db 301 DKSLRIWREDEGNARLNMLSYNMRGELAENS DARGWEPLPERRLDAFRAYNDWRGE 360

Qy 361 NCEP 364
Db 361 NCEP 364

RESULT 7
US-10-116-581-4
; Sequence 4, Application US/10116581
; Publication No. US20020137116A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: Murphy, Dennis
; APPLICANT: Ried, John
; TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE THEREOF
; FILE REFERENCE: DIVER1120-4
; CURRENT APPLICATION NUMBER: US/10/112,442
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/886,400
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 09/619,032
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/407,806
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 08/613,220
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Thermococcus alcaliphilus
; US-10-112-442-4

Query Match 99.5%; Score 1870; DB 13; Length 364;
Best Local Similarity 99.5%; Pred. No. 4.9e-165;
Matches 352; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRALVFGNLOQAYAIPKSEIPKVIKAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60
Db 1 LRALVFGNLOQAYAIPKSEIPKVIKAYIPVIETLKEEIPFGLNITGYTLKFLPKDID 60

Qy 61 LVKGIGIASDLIEIIGTSYTHAILPLPLPSRVEAQORDREVKEELFEVSPKGFWLPBELAY 120
Db 61 LVKGIGIASDLIEIIGTSYTHAILPLPLPSRVEAQORDREVKEELFEVSPKGFWLPBELAY 120

Qy 121 DP1PAIKDNGYEYLADGEAMLFSAHNSAIKPKPLYPHILKAOREKRFRYISYLLG 180
Db 121 DP1PAIKDNGYEYLADGEAMLFSAHNSAIKPKPLYPHILKAOREKRFRYISYLLG 180

Qy 181 LRELRAIAKLVLFEKGVTLKAVKDIIEAVPVWAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240
Db 181 LRELRAIAKLVLFEKGVTLKAVKDIIEAVPVWAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240

Db 361 NGEP 364

QY 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELENSELCLPSELKHSGRELYLRTSSWAP 300

Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELENSELCLPSELKHSGRELYLRTSSWAP 300

QY 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERLDAFRAIYNDWRGE 360

Db 301 DKSLRIWREDEGNARLNMLSYNMRGELAFLAENS DARGWEPLPERLDAFRAIYNDWRGE 360

QY 361 NGEP 364

Db 361 NGEP 364

RESULT 9

US-10-112-418-4

; Sequence 4, Application US/10112418

; Publication No. US20020155486A1

; GENERAL INFORMATION:

; APPLICANT: DIVERSA CORPORATION

; APPLICANT: Murphy, Dennis

; APPLICANT: Ried, John

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND

FILE REFERENCE: DIVER1120-4

CURRENT APPLICATION NUMBER: US/10/112,418

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 09/886,400

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/619,032

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/407,806

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 08/613,220

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 364

TYPE: PRT

ORGANISM: Thermococcus alcaliphilus

US-10-114-083-4

Query Match 99.5%; Score 1870; DB 13; Length 364;

Best Local Similarity 99.5%; Pred. No. 4.9e-165;

Matches 362; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRALVFHGNLQYAEIPKSEIPKVIKEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDID 60

Db 1 LRALVFHGNLQYAEIPKSEIPKVIKEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDID 60

QY 61 LVKGIGIASDLIEIIGTSYTHAILPLLPLSRVEAQVORDREVKEELFEVSPKGFWLP ELAY 120

Db 61 LVKGIGIASDLIEIIGTSYTHAILPLLPLSRVEAQVORDREVKEELFEVSPKGFWLP ELAY 120

QY 121 DPIPAILKDNGYEYLFDAGEAMLFSAHNSAIKPKLYPHLIKAOREKRFRYISYLLG 180

Db 121 DPIPAILKDNGYEYLFDAGEAMLFSAHNSAIKPKLYPHLIKAOREKRFRYISYLLG 180

QY 181 LRELRAIKLVFEGKVTLKAVKDI EAVPVWAVNTAVMLGIGRLPLMNPKVVASWIEDKD 240

Db 181 LRELRAIKLVFEGKVTLKAVKDI EAVPVWAVNTAVMLGIGRLPLMNPKVVASWIEDKD 240

QY 121 DPIPAILKDNGYEYLFDAGEAMLFSAHNSAIKPKLYPHLIKQREKRFRYISYLG 180

Db 121 DPIPAILKDNGYEYLFDAGEAMLFSAHNSAIKPKLYPHLIKQREKRFRYISYLG 180

QY 181 LRELRAIKLVFEGKVTLKAVKDI EAVPVWAVNTAVMLGIGRLPLMNPKVVASWIEDKD 240

Db 181 LRELRAIKLVFEGKVTLKAVKDI EAVPVWAVNTAVMLGIGRLPLMNPKVVASWIEDKD 240

QY 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELENSELCLPSELKHSGRELYLRTSSWAP 300

Db 241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELENSELCLPSELKHSGRELYLRTSSWAP 300

RESULT 11

US-10-282-122A-53281

; Sequence 53281, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

Query Match ; Sequence 23237, Application US/10369493
 Best Local Similarity 5.6%; Score 105.5; DB 15; Length 573;
 Matches 77; Conservative 57; Mismatches 97; Indels 131; Gaps 19;

QY ; Publication No. US20030233675A1
 6 FHGNL-QYAEIPKS---EIPKVIKEAYIPV-----IETL 35
 Db 290 FLGLGKLGGVPSLGLSGEVPPVSPSPYWCPPGISTCPSIAAVTQSPNNSIETL 349

Query Match ; Sequence 23237, Application US/10369493
 Best Local Similarity 5.6%; Score 105.5; DB 15; Length 573;
 Matches 77; Conservative 57; Mismatches 97; Indels 131; Gaps 19;

QY ; Publication No. US20030233675A1
 6 FHGNL-QYAEIPKS---EIPKVIKEAYIPV-----IETL 35
 Db 290 FLGLGKLGGVPSLGLSGEVPPVSPSPYWCPPGISTCPSIAAVTQSPNNSIETL 349

RESULT 13 ; Sequence 175517, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21 (53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 175517
 LENGTH: 573
 TYPE: PRT
 ORGANISM: Glycine max

Query Match ; Sequence 23237, Application US/10369493
 Best Local Similarity 5.6%; Score 105.5; DB 15; Length 573;
 Matches 77; Conservative 57; Mismatches 97; Indels 131; Gaps 19;

QY ; Publication No. US20030233675A1
 6 FHGNL-QYAEIPKS---EIPKVIKEAYIPV-----IETL 35
 Db 290 FLGLGKLGGVPSLGLSGEVPPVSPSPYWCPPGISTCPSIAAVTQSPNNSIETL 349

RESULT 12 ; Sequence 47374, Application US/10282122A
 ; Publication No. US200202122A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; Title of Invention: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10 (52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 23237
 LENGTH: 312
 TYPE: PRT
 ORGANISM: Bacillus subtilis

Query Match ; Sequence 47374, Application US/10282122A
 Best Local Similarity 5.6%; Score 109; DB 15; Length 312;
 Matches 44; Conservative 32; Mismatches 58; Indels 56; Gaps 9;

QY ; Sequence 175517, Application US/10424599
 10 LQYAEIPKSEIPK-----VIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIDL 61
 Db 130 M-YAVVKYESGFPKERVIGQSGLVDTAR--FRTFVAEE---LNLS-----VKDVITGP 175
 QY ; Sequence 175517, Application US/10424599
 62 VKGIGIASDLIEIGTSYTHAI-LPLPLSRVEAQVQNDREVKEELFEVSPKG-FWLPE 117
 Db 176 VLGCGHGDMMVPLVRYSYAGGIPLETLPKERIDAVERTRKGGEIVNLNGNSAYYAPA 235
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 53281
 LENGTH: 890
 TYPE: PRT
 ORGANISM: Clostridium difficile
 US-10-282-122A-53281

Query Match ; Sequence 175517, Application US/10424599
 Best Local Similarity 5.9%; Score 111.5; DB 15; Length 890;
 Matches 72; Conservative 48; Mismatches 98; Indels 87; Gaps 16;

QY ; Sequence 175517, Application US/10424599
 53 FLPKDIDLVKGIGIASDLIEIGTSYTHAI-LPLPLSRVEAQVQNDREVKEELFEVSPKG 112
 Db 562 FQP-DLIAVGGSAMDAGKIMWVMEHPEVDFQDIA---MRPMDIRKRVY-VFPK- 612
 QY ; Sequence 175517, Application US/10424599
 113 FWLPELAYDPIP-----AIL-KDNGYEYLADGEAMLFSFAHLSAIKPIK 158
 Db 613 --MGEKAYFAAIPTSAGTSEVTTPFAVITDQDSGVKYPLADYELMPNNMAIIDADMMMEMP 670
 QY ; Sequence 175517, Application US/10424599
 159 LYPLH-----IKAQREKFRYISYL-----LGLRELRAIKLUVF-----GKVTL 198
 Db 671 --PRLTAAASGVDALTHALEAYVSMRLRTEPADGLL---QAGKIIFEYLPRAYKNGKNDK 724
 QY ; Sequence 175517, Application US/10424599
 199 KAVKDIEAVPVWAVNTA-----VMLGIGRLPLM-----P 229
 Db 725 EARKEKMASTWAGMSFANAFLGICHSLAHKLAGFHVOHGVANALLNEVIKFNAEAP 784
 QY ; Sequence 175517, Application US/10424599
 230 KKVASWIEDK-DNLLYGTIDEPFIGYDIAGY--RMSVEGLLEVIDBLNSELCLPSELK 285
 Db 785 NKMGAFSQYRVDCTIORYA--EFASFAGIKGSTDQEVDNLKAIDELKAKVGLPTK 841

Qy 36 IKEETPFGLNITGYTLKLPKDIDLVKGGLIASDLIRIGTSYTHAILPLPLSRVEAQV 95
Db 350 ---PPPSGASSLLANPLS-----VNLL-----DPVQPLGTSMDFP--PFLP---DPLV 388
Qy 96 ORDREVKEELFEVSPKGFWLPELAYDPI--IPAI-LKDNGYEYLFADEAMLFSAHNSA 152
Db 389 RMSLPLTSQQIPTFTP-----LMCDPTIVHVPVIDVCSSGQGYLVSGPAMSPS----- 435
Qy 153 IKPKIPLYPHLIKAQREKFRYISYLLGLRELRLKAIKLVFEG-----KVTLKAVKD 203
Db 436 ---IPPLHPLNVLVKPLIPESDAVV-----KGARETRLLLSGSSQGNQMRDTLPAT-- 484
Qy 204 IEAVPVWVAVNTAVMLGIGRPLMNPKKVASWIEDKDNILLYGTIDFIGYRDI----- 257
Db 485 -----LTNP-----LTNP-----ENQNNILVAGSRGLYTGTRDINAANS 516
Qy 258 --AGYRMSVEGLLEVDELNSELCLPSELKHSGRELYLRTSSWAPDKSLRIWREDEGNAR 315
Db 517 IARMGLVLSGSVSKVDSCGVYSELIC-----ENYGNLEAVKSN--DGGGAFLDDEGGSS 568
Qy 316 LN 317
Db 569 LD 570

RESULT 14

US-10-425-114-55544 Application US/10425114

; Sequence 55544, Application US/10425114

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovacic, David K.

; APPLICANT: Screeen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Title of Invention: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 55544

; LENGTH: 730

; TYPE: PRT

; FEATURE: ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY109F02_FBI.pep

US-10-425-114-55544

Query Match 5.6%; Score 105.5; DB 15; Length 730;
Best Local Similarity 21.3%; Pred. No. 1.3; Matches 77; Conservative 57; Mismatches 97; Indels 131; Gaps 19;

Qy 6 FHGNL-QYAEIPKS----EIPKVIKAYIPV-----IETL 35
Db 447 FLGLGLKLGKVSSLGSGEVPPIVSPIFSPYCWCPGPGISTCPSTIAVTQSPNNSIETL 506
Qy 36 IKEBIPFGLNITGYTLKLPKDIDLVKGGLIASDLIEITGTSYTHAILPLPLSRVEAQV 95
Db 507 ---PPPSGASLLANPLS-----VNLL-----DPVQPLGTSMDFP--PFLP---DPLV 545
Qy 96 ORDREVKEELFEVSPKGFWLPELAYDPI--IPAI-LKDNGYEYLFADEAMLFSAHNSA 152
Db 546 RMSLPLTSQQIPTFTP-----LMCDPTIVHVPVIDVCSSGQGYLVSGPAMSPS----- 592
Qy 153 IKPKIPLYPHLIKAQREKFRYISYLLGLRELRLKAIKLVFEG-----KVTLKAVKD 203
Db 593 ---IPPLHPLNVLVKPLIPESDAVV-----KGARETRLLLSGSSQGNQMRDTLPAT-- 641
Qy 204 IEAVPVWVAVNTAVMLGIGRPLMNPKKVASWIEDKDNILLYGTIDFIGYRDI----- 257

RESULT 15

US-09-815-242-12361

; Sequence 12361, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

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; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

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NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12361

LENGTH: 1073

TYPE: PRT

ORGANISM: Staphylococcus aureus

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Query Match 5.5%; Score 103; DB 9; Length 1073;
Best Local Similarity 21.2%; Pred. No. 4; Matches 58; Conservative 48; Mismatches 90; Indels 78; Gaps 15;

Qy 107 EVSPKGFWLPELAYDPIIPAIKLDNGYEYLFADEAMLFSAHNSAIKPKIPLYPHLIKA 166
Db 309 EISP-----YYDSL--LVKLSTHAISFKQAEEKMVRSLREMIRGVKTNIPFLINV 357
Qy 167 QREKR-----RYISYLLGLRELRLKAI-----KLVEGKVLKAVKDIE----- 205
Db 358 MKNKKFTSGDYTKPIEETPELFEDIOPSLDRGKTLEYIGNTINGFPNVEKRPKPDYEL 417
Qy 206 -AVPVWVAVNTAVMLGIGR-LPLMNPKVVASWIEDKDNILLYGTIDF-IGYRDIAGYRM 262
Db 418 ASIPTVSSSKIASFSGTKQQLDEVGPKGVAEWKKQDDVLL-TDTTFRDAHQSSLATRV 475
Qy 263 SVEGLLEVDELNSELCLPSELKHSGRELYLRTSSWAPDK-SLRIWREDEGNARLNMSY 321
Db 476 RTKDMINTIAS-----KTADVFKDGFSLEMW---GGATFD-VAY 509
Qy 322 NMRGELAFLAENSNDARWEPPLPERRLDAFRAINY 355

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us-09-619-032a-4.rapb

Db 510 N-----FLKENP---WERLERLR---KAIPN 529

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